

| | | |
|------------|--|-----|
| HUZZSIG37 | MGSRGQGLLLLAYCLLLAFASG-----LVLSRVPHVQGEQQEWEGT ; | 40 |
| zacrps | MAAPALLLLALLLPVGA-----WPGLPRRP----- ; | 25 |
| ACR3_HUMAN | MLLLGAVLLLLLALP-----GHDQETTTQGPVLLPLPK ; | 33 |
| HUZZSIG39 | MRPLLVL LLLGLAAG-----SPPLDDNKIPSLCP----- ; | 29 |
| C1QC_HUMAN | MDVGPSSLP HLGLKLLLLLLLLLALRGQA--NTGCY----- ; | 33 |
| | | |
| HUZZSIG37 | EELPSPPDHAERAEQEHEKYRPSQDQGLPASRCLRCCDPGTSMPATAV- ; | 89 |
| zacrps | -----CVHCCRPAPWPPGPYARVS ; | 43 |
| ACR3_HUMAN | GACTGWMA----- ; | 41 |
| HUZZSIG39 | ----- ; | 29 |
| C1QC_HUMAN | ----- ; | 33 |
| | | |
| HUZZSIG37 | -----PQINITILK----- ; | 98 |
| zacrps | DRDLWRGDLWRGLPRVRPTINIEILK----- ; | 69 |
| ACR3_HUMAN | -----GIPGHPPGHN ; | 50 |
| HUZZSIG39 | -----GHPGLPGTPGHH ; | 41 |
| C1QC_HUMAN | -----GIPGMPGLPGAPGKDG YDGLPGPK ; | 57 |
| | | |
| HUZZSIG37 | -----GEKGDGRDRLQ GKYGKTGSAGARGHTGPKGQKGS ; | 133 |
| zacrps | -----GEKGEAGVRGRAGRSKGGPPGARGLQGRRGQKQ ; | 104 |
| ACR3_HUMAN | GAPGRDGRDGTPEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGR ; | 100 |
| HUZZSIG39 | GSQGLPGRDGRDGRDGAPGAPGEKGGPRPLPGPRGDPGRGEAGPAGP ; | 91 |
| C1QC_HUMAN | GEPGIPAI PGIRGPKGQKGEPLPGHPGKNGPMGPPGMPGVPGPMGIPGE ; | 107 |
| | | |
| HUZZSIG37 | MGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIDTEFVNLYDHFNMTG ; | 183 |
| zacrps | VGPPGAACRRAYAAFSVGRREGLHSSDHFQAVPFDTEL VNL DGAFDLAAG ; | 154 |
| ACR3_HUMAN | KGEPGEGAYVYRSASFVG--LETYVTIPNMPIRFTKIFYNQNH YDGSTG ; | 148 |
| HUZZSIG39 | TGPAGECSVP PRSAFSAKRSESRVPPSPDAPLPFDRVLVNEQGHYDAVTG ; | 141 |
| C1QC_HUMAN | PGEEGRYKQKFQSVFTVTR-QTHQPPAPNSLIRFNAVL TN PQGDYDTSTG ; | 156 |
| | | |
| HUZZSIG37 | KFYCYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVG--DRSIM ; | 231 |
| zacrps | RFLCTVPGVYFLSLNVHTWNYKETYLHIMLNRRPAAVLYAQPS--ERSVM ; | 202 |
| ACR3_HUMAN | KFHCNIPGLYYFAYHITVY-MKDVKVSLFKKDKAMLFTYDQYQ--ENNVD ; | 195 |
| HUZZSIG39 | KFTCQVPGVYFAYVHATVY-RASLQFDLVKNGESIASFFQFFGGWPKPAS ; | 190 |
| C1QC_HUMAN | KFTCKVPGLYYFVYHASHT--ANLCVLLYRSGVKVVTFCGHTS--KTNQV ; | 202 |
| | | |
| HUZZSIG37 | QSQ-SLMLELREQDQVWVRLYK-GERENAI FSEELDTYITFSGYLVKHAT ; | 279 |
| zacrps | QAQ-SLMLLLAAGDAVWVRMFQ-RDRDNAIYGEHGDLYITFSGH LVKPAA ; | 250 |
| ACR3_HUMAN | QASGSVLLHLEVGDQVWLQVYGEGER-NGLYADN-DNDSTFTGFLLYHDT ; | 243 |
| HUZZSIG39 | LSG-GAMVRLEPEDQVWVQVGV-GDY-IGIYASI-KTDSTFSGFLVYSDW ; | 236 |
| C1QC_HUMAN | NSG-GVLLRLQVGEEVWLAVNDYYDM-VGIQGS D----SVFSGFLLFPD- ; | 245 |
| | | |
| HUZZSIG37 | EP----- ; | 281 |
| zacrps | EL----- ; | 252 |
| ACR3_HUMAN | N----- ; | 244 |
| HUZZSIG39 | HSSPVFA ; | 243 |
| C1QC_HUMAN | ----- ; | 245 |

FIGURE